

## RAW SEQUENCE LISTING

DATE: 01/07/2002

PATENT APPLICATION: US/09/378,261

TIME: 14:39:31

Input Set : N:\Crf3\RULE60\09378261.raw

Output Set: N:\CRF3\01072002\I378261.raw

#9

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Fukudome, Kenji

6 Esmon, Charles T.

8 (ii) TITLE OF INVENTION: Cloning and Regulation of an Endothelial

9 Cell Protein C/Activated Protein C Receptor

11 (iii) NUMBER OF SEQUENCES: 6

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Patrea L. Pabst

15 (B) STREET: 2800 One Atlantic Center, 1201 West Peachtree

16 Street

17 (C) CITY: Atlanta

18 (D) STATE: Georgia

19 (E) COUNTRY: US

20 (F) ZIP: 30306-3450

ENTERED

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28 (vi) CURRENT APPLICATION DATA:

C--&gt; 29 (A) APPLICATION NUMBER: US/09/378,261

C--&gt; 30 (B) FILING DATE: 20-Aug-1999

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 08/289,699

35 (B) FILING DATE: 12-AUG-1994

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Pabst, Patrea L.

40 (B) REGISTRATION NUMBER: 31,284

41 (C) REFERENCE/DOCKET NUMBER: OMR152

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (404)873-8794

45 (B) TELEFAX: (404)873-8795

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 1302 base pairs

52 (B) TYPE: nucleic acid

53 (C) STRANDEDNESS: single

54 (D) TOPOLOGY: linear

56 (ii) MOLECULE TYPE: cDNA

58 (iii) HYPOTHETICAL: NO

60 (iv) ANTI-SENSE: NO

62 (ix) FEATURE:

63 (A) NAME/KEY: misc\_feature

64 (B) LOCATION: 1..1302

65 (D) OTHER INFORMATION: /note= "Nucleotides 25 through 738 encode the

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67 Endothelial Cell Protein Receptor of Sequence ID No. 2."

69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

71	CAGGTCCGGA	GCCTCAACTT	CAGGATGTTG	ACAACATTGC	TGCCGATACT	GCTGCTGTCT	60
73	GGCTGGGCTT	TTTGTAGCCA	AGACGCCTCA	GATGGCCTCC	AAAGACTTCA	TATGCTCCAG	120
75	ATCTCCTACT	TCCGCGACCC	CTATCACGTG	TGGTACCAGG	GCAACGCGTC	GCTGGGGGGA	180
77	CACCTAACGC	ACGTGCTGGA	AGGCCCAGAC	ACCAACACCA	CGATCATTCA	GCTGCAGCCC	240
79	TTGCAGGAGC	CCGAGAGCTG	GGCGCGCACG	CAGAGTGGCC	TGCAGTCCTA	CCTGCTCCAG	300
81	TTCCACGGCC	TCGTGCGCCT	GGTGCAACAG	GAGCGGACCT	TGGCCTTTCC	TCTGACCATC	360
83	CGCTGCTTCC	TGGGCTGTGA	GCTGCCTCCC	GAGGGCTCTA	GAGCCCATGT	CTTCTTCGAA	420
85	GTGGCTGTGA	ATGGGAGCTC	CTTTGTGAGT	TTCCGGCCGG	AGAGAGCCTT	GTGGCAGGCA	480
87	GACACCCAGG	TCACCTCCGG	AGTGGTCAAC	TTCAACCCTG	AGCAGCTCAA	TGCCTACAAC	540
89	CGCACTCGGT	ATGAACTGCG	GGAATTCCTG	GAGGACACCT	GTGTGCAGTA	TGTGCAGAAA	600
91	CATATTTCCG	CGGAAAACAC	GAAAGGGAGC	CAAAACAAGC	GCTCCTACAC	TTCGCTGGTC	660
93	CTGGGCGTCC	TGGTGGGCGG	TTTCATCATT	GCTGGTGTGG	CTGTAGGCAT	CTTCCTGTGC	720
95	ACAGGTGGAC	GGCGATGTTA	ATTACTCTCC	AGCCCCGTCA	GAAGGGGCTG	GATTGATGGA	780
97	GGCTGGCAAG	GGAAAGTTTC	AGCTCACTGT	GAAGCCAGAC	TCCCCAACTG	AAACACCAGA	840
99	AGGTTTGGAG	TGACAGCTCC	TTTCTTCTCC	CACATCTGCC	CACTGAAGAT	TTGAGGGAGG	900
101	GGAGATGGAG	AGGAGAGGTG	GACAAAGTAC	TTGTTTGCT	AAGAACCTAA	GAACGTGTAT	960
103	GCTTTGCTGA	ATTAGTCTGA	TAAGTGAATG	TTTATCTATC	TTTGTGAAA	ACAGATAATG	1020
105	GAGTTGGGGC	AGGAAGCCTA	TGCGCCATCC	TCCAAAGACA	GACAGAATCA	CCTGAGGCGT	1080
107	TCAAAAGATA	TAACCAAATA	AACAAGTCAT	CCACAATCAA	AATACAACAT	TCAATACTTC	1140
109	CAGGTGTGTC	AGACTTGGGA	TGGGACGCTG	ATATAATAGG	GTAAGAAAGAA	GTAACACGAA	1200
111	GAAGTGGTGG	AAATGTAAAA	TCCAAGTCAT	ATGGCAGTGA	TCAATTATTA	ATCAATTAAAT	1260
113	AATATTAATA	AATTTCTTAT	ATTTAAAAAA	AAAAAAAAAA	AA		1302

115 (2) INFORMATION FOR SEQ ID NO: 2:

116 (i) SEQUENCE CHARACTERISTICS:

117 (A) LENGTH: 238 amino acids

118 (B) TYPE: amino acid

119 (D) TOPOLOGY: linear

121 (ii) MOLECULE TYPE: protein

123 (iii) HYPOTHETICAL: NO

125 (ix) FEATURE:

126 (A) NAME/KEY: misc\_feature

127 (B) LOCATION: 1..365

128 (D) OTHER INFORMATION: /note= "Endothelial Cell Protein Receptor

129 encoded by

130 nucleotides 1 through 1302 of Sequence ID No. 1."

131 (ix) FEATURE:

132 (A) NAME/KEY: Modified-site

133 (B) LOCATION: 1..15

134 (D) OTHER INFORMATION: /note= "Amino acids 1-15 represent

135 a putative signal sequence."

137 (ix) FEATURE:

138 (A) NAME/KEY: Domain

139 (B) LOCATION: 211..236

140 (D) OTHER INFORMATION: /note= "Amino acids 211-236

141 represent a putative transmembrane domain."

143 (ix) FEATURE:

144 (A) NAME/KEY: Active-site

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145 (B) LOCATION: 47..174  
 146 (D) OTHER INFORMATION: /note= "Amino acids 47-49, 64-66,  
 147 136-138 and 172-174 represent potential  
 148 N-glycosylation sites."  
 150 (ix) FEATURE:  
 151 (A) NAME/KEY: Modified-site  
 152 (B) LOCATION: 17..186  
 153 (D) OTHER INFORMATION: /note= "Amino acids 17, 114, 118  
 154 and 186 represent extracellular cysteine  
 155 residues."  
 157 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 159 Met Leu Thr Thr Leu Leu Pro Ile Leu Leu Ser Gly Trp Ala Phe  
 160 1 5 10 15  
 162 Cys Ser Gln Asp Ala Ser Asp Gly Leu Gln Arg Leu His Met Leu Gln  
 163 20 25 30  
 165 Ile Ser Tyr Phe Arg Asp Pro Tyr His Val Trp Tyr Gln Gly Asn Ala  
 166 35 40 45  
 168 Ser Leu Gly Gly His Leu Thr His Val Leu Glu Gly Pro Asp Thr Asn  
 169 50 55 60  
 171 Thr Thr Ile Ile Gln Leu Gln Pro Leu Gln Glu Pro Glu Ser Trp Ala  
 172 65 70 75 80  
 174 Arg Thr Gln Ser Gly Leu Gln Ser Tyr Leu Leu Gln Phe His Gly Leu  
 175 85 90 95  
 177 Val Arg Leu Val His Gln Glu Arg Thr Leu Ala Phe Pro Leu Thr Ile  
 178 100 105 110  
 180 Arg Cys Phe Leu Gly Cys Glu Leu Pro Pro Glu Gly Ser Arg Ala His  
 181 115 120 125  
 183 Val Phe Phe Glu Val Ala Val Asn Gly Ser Ser Phe Val Ser Phe Arg  
 184 130 135 140  
 186 Pro Glu Arg Ala Leu Trp Gln Ala Asp Thr Gln Val Thr Ser Gly Val  
 187 145 150 155 160  
 189 Val Thr Phe Thr Leu Gln Gln Leu Asn Ala Tyr Asn Arg Thr Arg Tyr  
 190 165 170 175  
 193 Glu Leu Arg Glu Phe Leu Glu Asp Thr Cys Val Gln Tyr Val Gln Lys  
 194 180 185 190  
 196 His Ile Ser Ala Glu Asn Thr Lys Gly Ser Gln Thr Ser Arg Ser Tyr  
 197 195 200 205  
 200 Thr Ser Leu Val Leu Gly Val Leu Val Gly Gly Phe Ile Ile Ala Gly  
 201 210 215 220  
 203 Val Ala Val Gly Ile Phe Leu Cys Thr Gly Gly Arg Arg Cys  
 204 225 230 235  
 206 (2) INFORMATION FOR SEQ ID NO: 3:  
 208 (i) SEQUENCE CHARACTERISTICS:  
 209 (A) LENGTH: 244 amino acids  
 210 (B) TYPE: amino acid  
 211 (C) STRANDEDNESS: single  
 212 (D) TOPOLOGY: linear  
 214 (ii) MOLECULE TYPE: peptide  
 216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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```

218 Met Leu Thr Lys Phe Leu Leu Leu Leu Leu Leu Leu Leu Pro Gly Cys
219 1 5 10 15
221 Ala Phe Val Thr Pro Met Ala Pro Lys Ala Ala Tyr Ala Pro Asp Leu
222 20 25 30
224 Leu Phe Pro Arg Pro Pro Ser Cys Glu Ala Ser Gly Gln Arg Ser Leu
225 35 40 45
227 Gly Lys Leu Leu Thr His Thr Leu Glu Gly Pro Ser Gln Asn Val Thr
228 50 55 60
230 Ile Leu Gln Leu Gln Pro Trp Gln Asp Pro Glu Ser Trp Glu Arg Thr
231 65 70 75 80
233 Glu Ser Gly Leu Gln Ile Tyr Leu Thr Gln Phe Glu Ser Leu Val Lys
234 85 90 95
236 Leu Val Tyr Arg Glu Arg Lys Glu Asn Val Phe Phe Pro Leu Thr Val
237 100 105 110
239 Ser Cys Ser Leu Gly Cys Glu Leu Pro Glu Glu Glu Glu Glu Gly Ser
240 115 120 125
242 Glu Pro His Val Phe Phe Asp Val Ala Val Asn Gly Ser Ala Phe Val
243 130 135 140
245 Ser Phe Arg Pro Lys Thr Ala Val Trp Val Ser Gly Ser Gln Glu Pro
246 145 150 155 160
248 Ser Lys Ala Ala Asn Phe Thr Leu Lys Gln Leu Asn Ala Tyr Asn Arg
249 165 170 175
251 Thr Arg Tyr Glu Leu Gln Glu Phe Leu Gln Asp Thr Cys Val Glu Phe
252 180 185 190
255 Leu Glu Asn His Ile Thr Thr Gln Asn Met Lys Gly Ser Gln Thr Gly
256 195 200 205
258 Arg Ser Tyr Thr Ser Leu Val Leu Gly Ile Leu Met Gly Cys Phe Ile
259 210 215 220
261 Ile Ala Gly Val Ala Val Gly Ile Phe Met Cys Thr Ser Gly Arg Gly
262 225 230 235 240
264 Leu Leu Ile Ile

```

## 267 (2) INFORMATION FOR SEQ ID NO: 4:

## 269 (i) SEQUENCE CHARACTERISTICS:

270 (A) LENGTH: 335 amino acids

271 (B) TYPE: amino acid

272 (C) STRANDEDNESS: single

273 (D) TOPOLOGY: linear

## 275 (ii) MOLECULE TYPE: peptide

## 278 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

280 Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
281 1 5 10 15
283 Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln
284 20 25 30
286 Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala
287 35 40 45
289 Trp Leu Gly Glu Leu Gln Thr His Ser Trp Ser Asn Asp Ser Asp Thr
290 50 55 60
292 Val Arg Ser Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln
293 65 70 75 80

```

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```

295   Trp Glu Thr Leu  Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr
296                        85                      90                      95
298   Arg Asp Val  Lys Glu Phe Ala Lys Met Leu Arg Leu Ser Tyr Pro Leu
299                        100                     105                     110
301   Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala Ser
302                        115                     120                     125
304   Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe
305                        130                     135                     140
307   Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val Asn
308   145                      150                      155                      160
310   Leu Ala Ile Gln Val Leu Asn Gln Asp Lys Trp Thr Arg Glu Thr Val
311                        165                      170                      175
313   Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu
314                        180                      185                      190
317   Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala Trp
318                        195                      200                      205
320   Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Leu Val Cys
321                        210                      215                      220
323   His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met Arg
324   225                      230                      235                      240
326   Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn
327                        245                      250                      255
329   Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala Gly
330                        260                      265                      270
332   Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly
333                        275                      280                      285
335   Gln Asp Ile Val Leu Tyr Trp Gly Gly Ser Tyr Thr Ser Met Gly Leu
336   290                      295                      300
338   Ile Ala Leu Ala Val Leu Ala Cys Leu Leu Phe Leu Leu Ile Val Gly
339   305                      310                      315                      320
341   Phe Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Gly Val Leu
342                        325                      330                      335

```

344 (2) INFORMATION FOR SEQ ID NO: 5:

346 (i) SEQUENCE CHARACTERISTICS:

347 (A) LENGTH: 336 amino acids

348 (B) TYPE: amino acid

349 (C) STRANDEDNESS: single

350 (D) TOPOLOGY: linear

352 (ii) MOLECULE TYPE: peptide

355 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

357   Met Arg Tyr Leu Pro Cys Leu Leu Leu Trp Ala Phe Leu Gln Val Trp
358   1          5          10          15
360   Gly Gln Ser Glu Val Gln Gln Lys Asn Tyr Thr Phe Arg Cys Leu Gln
361                        20          25          30
363   Thr Ser Ser Phe Ala Asn Ile Ser Trp Ser Arg Thr Asp Ser Leu Ile
364                        35          40          45
366   Leu Leu Gly Asp Leu Gln Thr His Arg Trp Ser Asn Asp Ser Ala Thr
367   50          55          60
369   Ile Ser Phe Thr Lys Pro Trp Ser Gln Gly Lys Leu Ser Asn Gln Gln

```

VERIFICATION SUMMARY

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]